

Fig. 1

1	AGCTCACAGCC	11
12	ATGGTTACCTTCAGCCACGTCTCCAGTCTGAGTCACTGGTTCCTCTTGCTGCTGCTGCTG	71
1	<u>M V T F S H V S S L S H W F L L L L L</u>	20
72	AATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGAT	131
21	<u>N L F L P V I F A M P E S Y S F N C P D</u>	40
132	GGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAG	191
41	G E Y Q S N D V C C K T C P S G T F V K	60
192	GCGCCCTGCAAAATCCCCATACTCAAGGACAATGTGAGAAGTGTACCCAGGAACATTC	251
61	A P C K I P H T Q G Q C E K C H P G T F	80
252	ACAGGGAAAGATAATGGCCTGCATGATTGTGAACCTTTGCTCCACCTGTGATAAAGACCAG	311
81	T G K D N G L H D C E L C S T C D K D Q	100
312	AATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAAATGCGAGTGCCAAATAGGTCTT	371
101	N M V A D C S A T S D R K C E C Q I G L	120
372	TACTACTATGACCCAAAATTTCCGGAATCATGCCGCCCATGTACCAAGTGTCCCAAGGA	431
121	Y Y Y D P K F P E S C R P C T K C P Q G	140
432	ATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTTCATCTGTTTCA	491
141	I P V L Q E C N S T A N T V C <u>S S S V S</u>	160
492	AATCCCAGAACTGGCTGTTCTCTACTGATGCTAATTGTCTTCTGTATCTGA	542
161	<u>N P R N W L F L L M L I V F C I *</u>	177
543	AGAAGATAAAGGTTCTACAGATGGTGTCTGTAGCTTCCTTTTATTGCTGTGAAGAGAA	600
601	ACCATGGAGGCAACTCTTTTATTTTATTTTATTTTAAATGTCTTGAACCTTGATTTGAAG	660
661	ACCAGGCTGGACTCAAACCTCACAGAGATCCGGACTAGGCACCTCTAATATAGGAAAACAT	720
721	TGAATTGGGACTGGCTTACAGTTTCAGAAGTTCTGTCCATGATTATCATAGTGCGAAGCA	780
781	TGGAGGCACGGAGGCACACATGGTGTGGAAGAAGAAGCTGAGAGTTCTGCATCTTGATCT	840
841	GCAAGCAATAAAAGGAGACTGTGTGCCACACTACACATAGCTTGAACATAGGAGACCTCA	900
901	AAGCCTGTCCCCACAGTGACAACTTCCTCCAACAAGGTCATACCTCCTAATAATACCAT	960
961	TTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAC	1020
1021	CACAGGTTAAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCCTTGAGAGTAAGTAA	1080
1081	CAATTTAGATGAAGGCAAGTCCTGGTATCAGGTCCAAAAGAACTCAGGATGAATGGTCC	1140
1141	ACTGTGGTTCCTATTAACATACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCAC	1200
1201	TGGCTTCCCTTCCCCTAGCTTCTCATTCCCAGGTAACCCTGCCATTTTTTGGTAATGTGC	1260
1261	CTTCTTGGTTCCTCTCCTTTCCCCCTCTCTTCTGGTCTTATTTCTCTTCTCTCCC	1320
1321	ACTCTCCACCAGCCGCTCTTAAGGCCTGAGTCAGTCTGCAGGCCATGTTTAATCTACTA	1380
1381	CTTCTCTCTGCTCTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCCTATCTACA	1440
1441	ATAAACCTTCCCCTAACAGAAATGGAACAGTTTTGTCTCACTTTGTACATCTGGTG	1500
1501	CCTGAAACC	1509

Fig. 2

7F4 GPDGEY---QSN_DVC CKTCPSGT_FVKAPGK IPHTQGQGEKCHPGT FTGKD_NGLHDGELCS 60
mTNFR CPGGKYVHSKNNSIG GTKCHKGT_YLVSDCP SPGRDTVCREGEKGT FTASQ_NYLRQCLSK 60

7F4 TCDKD--QNMVADGS ATSDRKGEC---QIG LYYYDPKFPESGRPC TKCPQGIPVLQEGNS 120
mTNFR TGRKEMSQVEISPCQ ADKDTVGGKENQFQ RYLSETHEQ--GVDC SPCFNGTVTIP-GKE 120

7F4	<u>TANTVC</u>	126
mTNFR	<u>TQNTVC</u>	126

Fig. 3

testis
kidney
skeletal muscle

liver

lung

spleen

brain

heart



Fig. 4

peripheral blood leukocyte

colon

small intestine

ovary

testis

prostate gland

thymus

spleen

pancreas

kidney

skeletal muscle

liver

lung

placenta

brain

heart

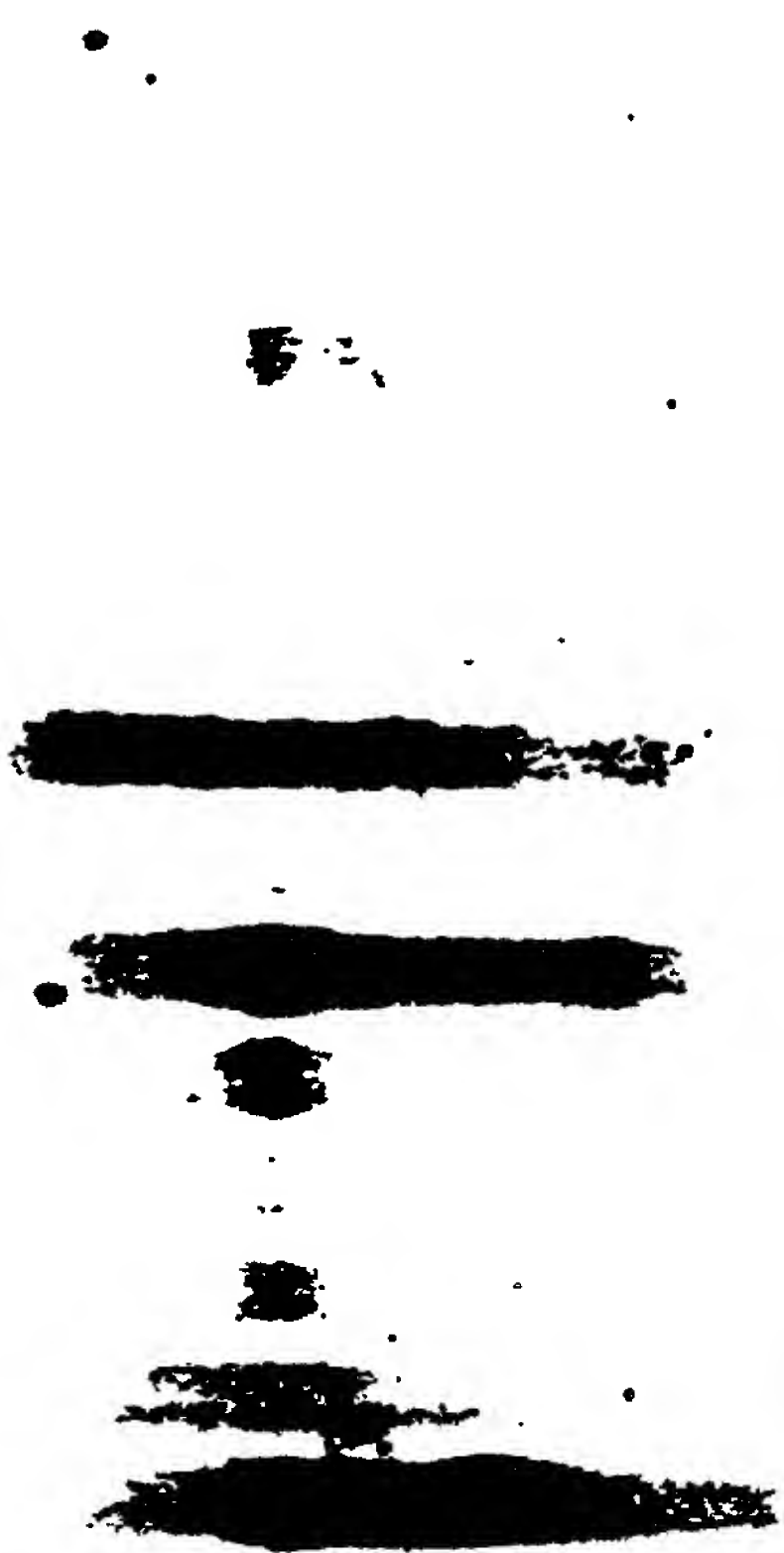


Fig. 5A



Fig. 5B

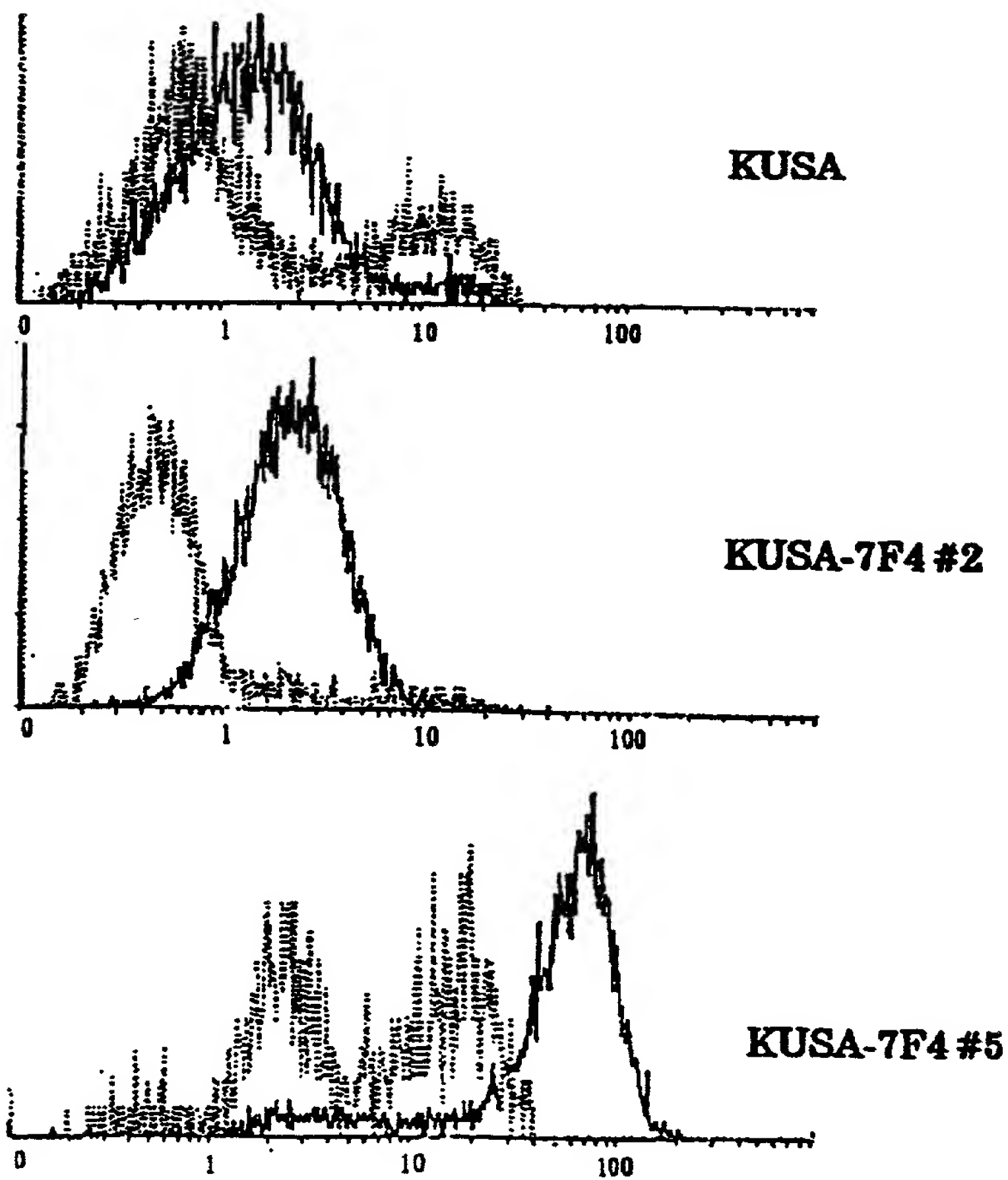


Fig. 6

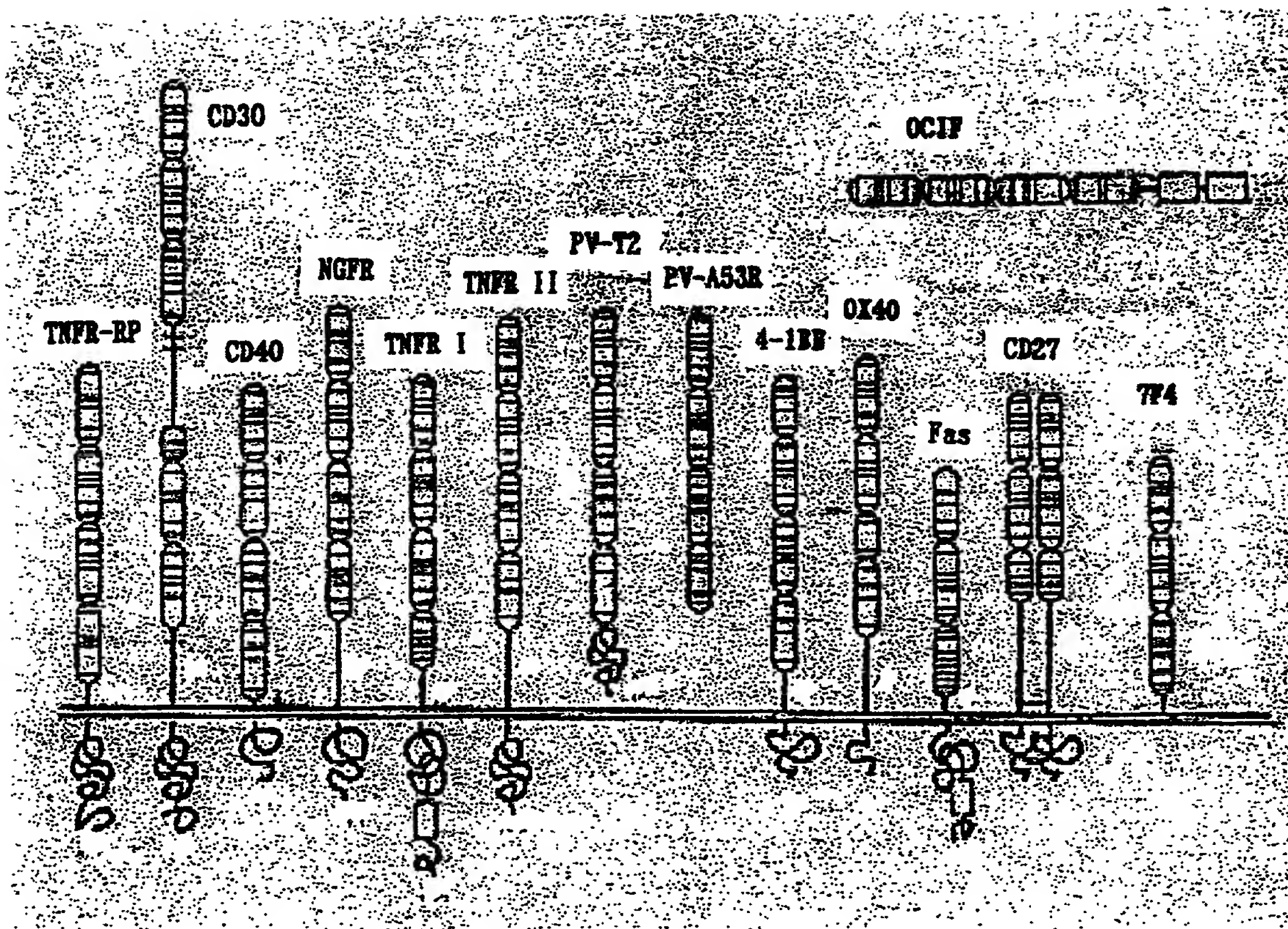


Fig. 7

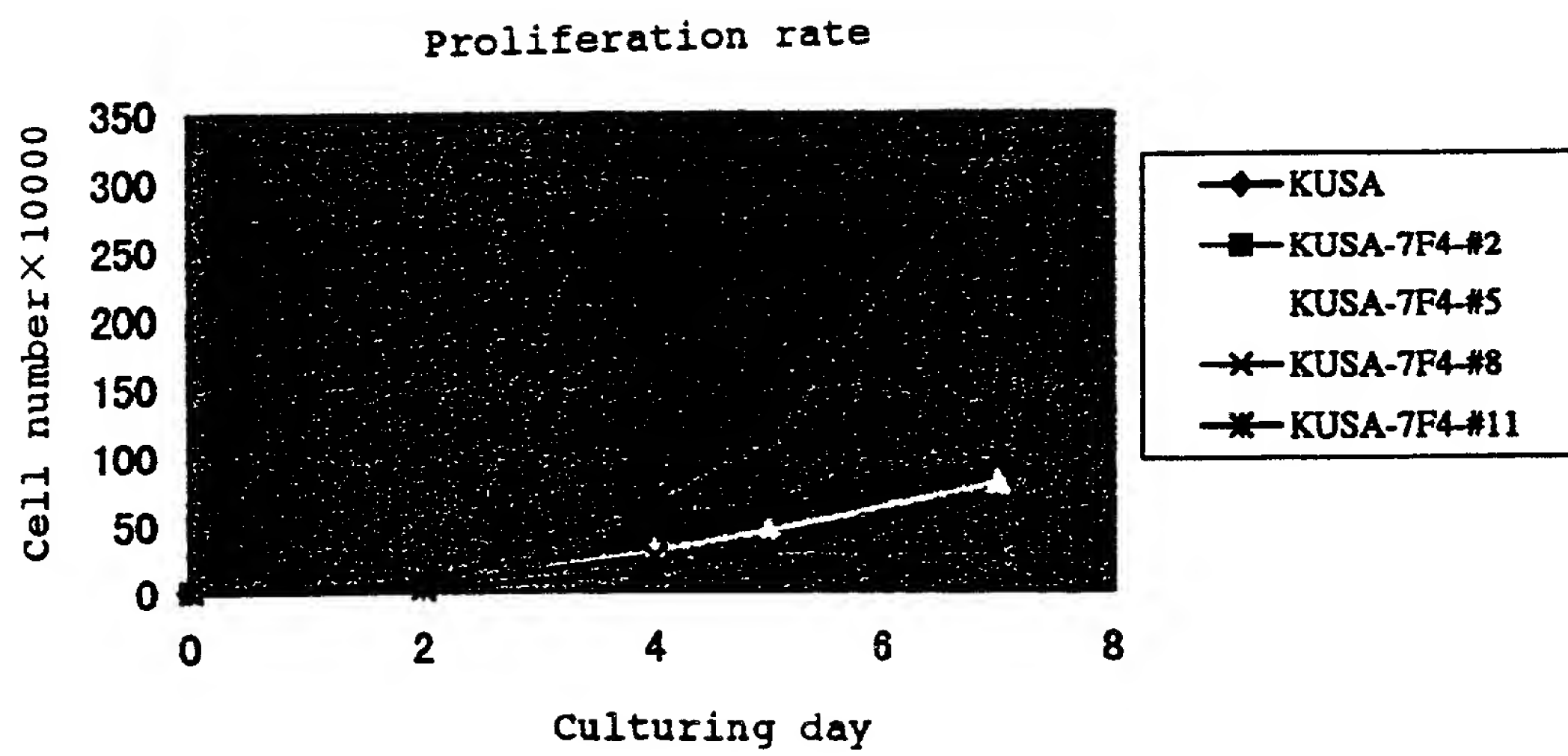


Fig. 8

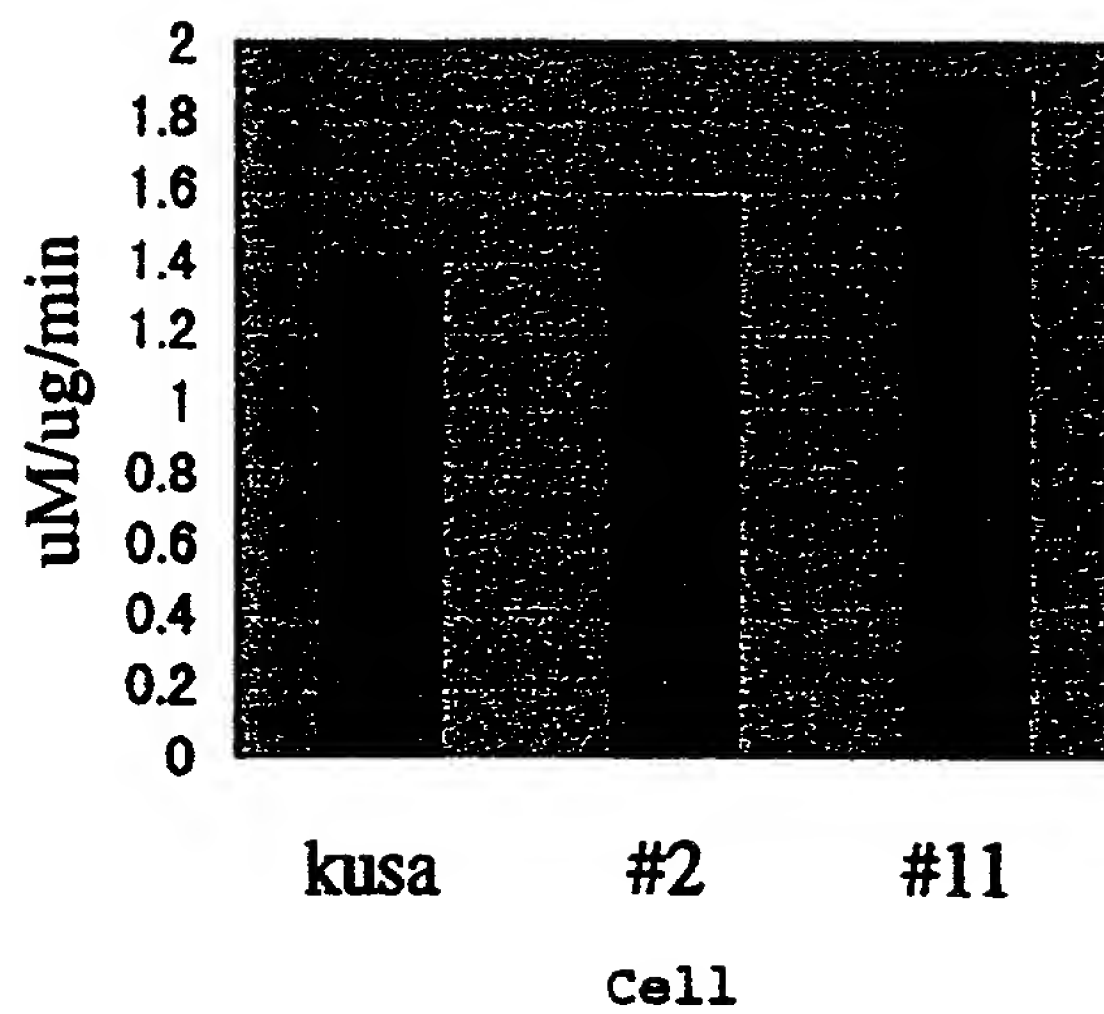


Fig. 9

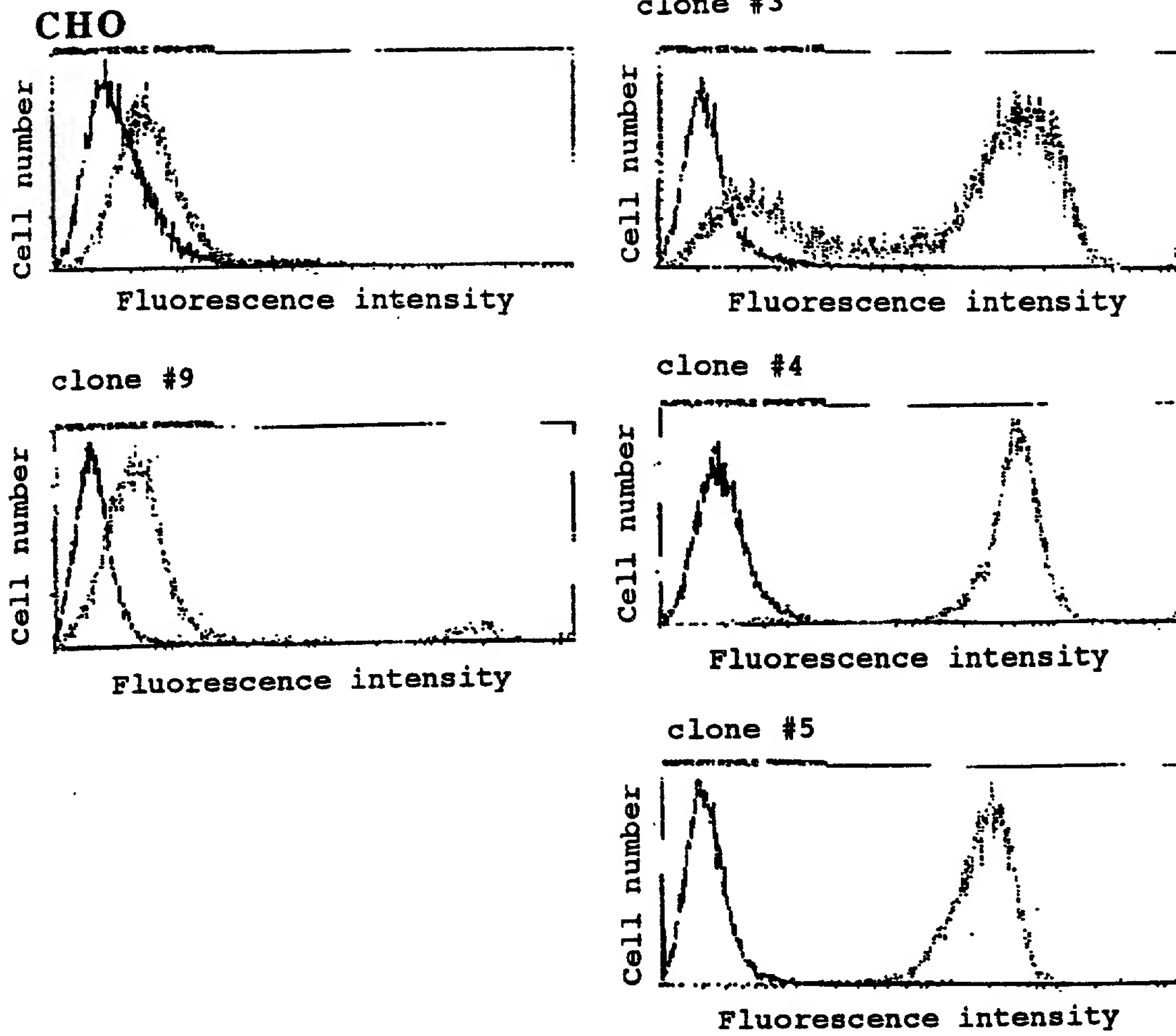


Fig. 10

